EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	2	"20030224353"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/23 14:48
L2	2703	sars or hsars or hcov	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/23 14:49
L3	396	full adj genom$	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/23 14:53
L4	4	2 with 3	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/23 14:49
L5	13706	full with genom$	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/23 14:50
L6	8	2 with 5 not 4	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/23 14:50
L7	16	hku-39849 or hku adj "39849" or hku39849	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/23 14:56
L8	0	hku-39 or hku adj "39" or hku39	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/23 14:56

```
? ds

Set      Items    Description
S1       12902    CORONAVIR? OR CORONA(W)VIR?
S2       12936    CORONAVIR? OR CORONA(W)(VIRUS OR VIRUSES OR VIRAL)
S3       67616    CONSENSUS
S4          96    S3 AND S2
S5       33626    UNIVERSAL
S6     1318082    DETECT?
S7          38    S2 AND S6 AND (S3 OR S5)
S8    18643642    PY<2003
S9          20    S7 AND S8
S10       4726    SARS
S11         13    S7 AND S10
? log hold
       23jun06 09:32:46 User208669 Session D3044.3
             $0.13     0.039 DialUnits File155
     $0.13  Estimated cost File155
             $0.18     0.039 DialUnits File50
     $0.18  Estimated cost File50
             $0.88     0.039 DialUnits File357
     $0.88  Estimated cost File357
             OneSearch, 3 files,  0.118 DialUnits FileOS
     $0.02  TELNET
     $1.21  Estimated cost this search
     $1.21  Estimated total session cost   0.118 DialUnits
Logoff: level 05.12.03 D  09:32:46
```

```
=> d his

        (FILE 'HOME' ENTERED AT 08:31:59 ON 23 JUN 2006)

        FILE 'REGISTRY' ENTERED AT 08:32:07 ON 23 JUN 2006
L1          0 S (GGGACTATCCTAAGTGTGA OR TAACACACAACICCATCATCA)/SQN
L2         38 S (GGGACTATCCTAAGTGTGA OR TAACACACAACICCATCATCA)/SQSN
L3          0 S L1 AND SQL<100

        FILE 'CA' ENTERED AT 08:33:46 ON 23 JUN 2006
L4         26 S L2
L5         11 S L4 AND SARS
L6         15 S L4 NOT SARS
L7         11 S L4 AND PRIMER?
L8          2 S L4 AND CONSENSUS

=> log hold
COST IN U.S. DOLLARS                        SINCE FILE        TOTAL
                                              ENTRY          SESSION
FULL ESTIMATED COST                           42.74          105.93

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)   SINCE FILE        TOTAL
                                              ENTRY          SESSION
CA SUBSCRIBER PRICE                           -1.42           -1.42

 SESSION WILL BE HELD FOR 60 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 08:36:09 ON 23 JUN 2006
```

NCBI   megablast **BLAST**

Nucleotide   Protein   Translations   Retrieve results for an RID

What is Mega BLAST?

Search
```
atattaggttttttacctacccaggaaaagccaaccaacctcgatctcttgtagatctgtt
ctctaaacgaactttaaaatctgtgtagctgtcgctcggctgcatgcctagtgcacctac
gcagtataaacaataataaattttactgtcgttgacaagaaacgagtaactcgtccctct
tctgcagactgcttacggtttcgtccgtgttgcagtcgatcatcagcatacctaggtttc
gtccgggtgtgaccgaaaggtaagatggagagccttgttcttggtgtcaacgagaaaaca
```

Load query file
from disk   [   ]   Browse

Set subsequence   From: [   ]   To: [   ]

Choose database   [nr   ▼]

Return alignment
endpoints only   ☐

Now: **BLAST** or [   ] [   ]

Options for advanced blasting

Limit by entrez
query   [   ] or select from: [All organisms   ▼]

Choose filter   ☑ Low complexity ☐ Human repeats ☐ Mask for lookup table only ☐ Mask lower case

Expect   [10   ]

Word Size   [28 ▼]

Percent Identity,
match, mismatch
scores   [None, 1, -2 ▼]

Other advanced   [   ]

Format

Show   ☑ Graphical Overview ☑ Linkout ☑ Sequence Retrieval ☑ NCBI-gi [Alignment ▼] in [HTML ▼] format

☐ CDS feature

NCBI   *formatting* BLAST

Nucleotide   Protein   Translations   Retrieve results for an RID

Your request has been successfully submitted and put into the Blast Queue.

Query = (29,742 letters)

The request ID is 1151085824-31454-204534673121.BLASTQ4

[Format!] or [Reset]

The results are estimated to be ready in 10 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☑ Graphical Overview ☑ Linkout ☑ Sequence Retrieval ☑ NCBI-gi Alignment ▾ in HTML ▾ format

☐ CDS feature

Masking Character Lower Case ▾   Masking Color Grey ▾

Number of: Descriptions 100 ▾ Alignments 50 ▾ Graphic overview 100 ▾

Alignment view Hit Table ▾

Start formatting from query # [ ]

Limit results by entrez query [ ] or select from: All organisms ▾

Expect value range: [ ] [ ]

Results file ☐

NCBI   results of BLAST

```
# BLASTN 2.2.14 [May-07-2006]
# Query:
# Database: nr
# Fields: query id, subject ids, % identity, alignment length, mismatches, gap opens, q. star
# 50 hits found
```

		% identity	alignment length	mismatches	gap opens		q. star
1_31454	gi|30023963|gb|AY278491.2|	100.00	29727	0	0	1	29727	1
1_31454	gi|33115118|gb|AY323977.2|	99.97	29728	8	2	1	29727	1
1_31454	gi|30698326|gb|AY291451.1|	99.97	29728	8	2	1	29727	1
1_31454	gi|40548933|gb|AY502928.1|	99.97	29728	8	2	1	29727	1
1_31454	gi|40548897|gb|AY502925.1|	99.97	29728	8	2	1	29727	1
1_31454	gi|52546959|gb|AY714217.1|	99.96	29728	9	2	1	29727	1
1_31454	gi|30248028|gb|AY274119.3|	99.96	29728	9	2	1	29727	1
1_31454	gi|31873092|gb|AY321118.1|	99.96	29728	7	3	1	29727	1
1_31454	gi|40548921|gb|AY502927.1|	99.96	29728	11	2	1	29727	1
1_31454	gi|40548909|gb|AY502926.1|	99.96	29728	11	2	1	29727	1
1_31454	gi|40548945|gb|AY502929.1|	99.96	29728	10	2	1	29727	1
1_31454	gi|33518725|gb|AY362699.1|	99.96	29728	10	2	1	29727	1
1_31454	gi|40548969|gb|AY502931.1|	99.96	29728	11	2	1	29727	1
1_31454	gi|40548957|gb|AY502930.1|	99.96	29728	11	2	1	29727	1
1_31454	gi|33518724|gb|AY362698.1|	99.96	29728	11	2	1	29727	1
1_31454	gi|33411399|dbj|AP006557.1|	99.96	29728	11	2	1	29727	1
1_31454	gi|30027617|gb|AY278741.1|	99.95	29728	12	2	1	29727	1
1_31454	gi|31581502|gb|AY291315.1|	99.95	29728	12	2	1	29727	1
1_31454	gi|33578015|gb|AY310120.1|	99.95	29728	12	2	1	29727	1
1_31454	gi|40548981|gb|AY502932.1|	99.95	29728	13	2	1	29727	1
1_31454	gi|37576845|gb|AY427439.1|	99.97	29712	7	2	17	29727	1
1_31454	gi|38505491|gb|AY485278.1|	99.95	29728	10	4	1	29727	1
1_31454	gi|40548873|gb|AY502923.1|	99.95	29728	13	2	1	29727	1
1_31454	gi|37624341|gb|AY394998.1|	99.97	29713	8	2	16	29727	1
1_31454	gi|33411459|dbj|AP006561.1|	99.95	29728	13	2	1	29727	1
1_31454	gi|33411444|dbj|AP006560.1|	99.95	29728	13	2	1	29727	1
1_31454	gi|67003761|gb|AY864805.1|	99.95	29728	14	2	1	29727	1
1_31454	gi|38304867|gb|AY282752.2|	99.96	29713	9	2	16	29727	1
1_31454	gi|33411429|dbj|AP006559.1|	99.95	29728	14	2	1	29727	1
1_31454	gi|38231927|gb|AY350750.1|	99.96	29715	10	2	14	29727	1
1_31454	gi|30468042|gb|AY283794.1|	99.96	29712	9	2	17	29727	1
1_31454	gi|30468044|gb|AY283796.1|	99.96	29712	9	2	17	29727	1
1_31454	gi|33114202|gb|AY345987.1|	99.96	29713	10	2	16	29727	1
1_31454	gi|33114190|gb|AY345986.1|	99.96	29713	10	2	16	29727	1
1_31454	gi|33411414|dbj|AP006558.1|	99.94	29728	13	4	1	29727	1
1_31454	gi|38231932|gb|AY357075.1|	99.96	29714	9	4	15	29727	1
1_31454	gi|37361915|gb|AY283798.2|	99.96	29712	11	2	17	29727	1
1_31454	gi|38505482|gb|AY485277.1|	99.94	29728	13	3	1	29727	1
1_31454	gi|67003775|gb|AY864806.1|	99.94	29728	17	2	1	29727	1
1_31454	gi|37624333|gb|AY394990.1|	99.95	29713	12	2	16	29727	1
1_31454	gi|37624332|gb|AY394989.1|	99.95	29713	12	2	16	29727	1
1_31454	gi|33114214|gb|AY345988.1|	99.95	29713	12	2	16	29727	1
1_31454	gi|45644994|gb|AY559081.1|	99.95	29713	11	3	17	29727	4
1_31454	gi|45645004|gb|AY559087.1|	99.94	29712	16	2	17	29727	1
1_31454	gi|37624334|gb|AY394991.1|	99.95	29713	13	2	16	29727	1
1_31454	gi|45645007|gb|AY559088.1|	99.95	29714	12	4	17	29727	1
1_31454	gi|99078934|gb|DQ497008.1|	99.93	29728	20	2	1	29727	1
1_31454	gi|37624336|gb|AY394993.1|	99.95	29713	14	2	16	29727	1
1_31454	gi|37624335|gb|AY394992.1|	99.95	29713	14	2	16	29727	1
1_31454	gi|45645023|gb|AY559096.1|	99.95	29709	13	2	20	29727	12

NCBI   *nucleotide-nucleotide* **BLAST**

Nucleotide	Protein	Translations	Retrieve results for an RID

Search
```
atattaggttttttacctacccaggaaaagccaaccaacctcgatctcttgtagatctgtt
ctctaaacgaactttaaaatctgtgtagctgtcgctcggctgcatgcctagtgcacctac
gcagtataaacaataataaattttactgtcgttgacaagaaacgagtaactcgtccctct
tctgcagactgcttacggtttcgtccgtgttgcagtcgatcatcagcatacctaggtttc
gtccgggtgtgaccgaaaggtaagatggagagccttgttcttggtgtcaacgagaaaaca
```

Set subsequence   From: [   ]   To: [   ]

Choose database   [nr   ▼]

Now: (**BLAST**) or (Reset query) (Reset all)

Options for advanced blasting

Limit by entrez query   [   ] or select from: [All organisms   ▼]

Choose filter   ☑ Low complexity ☐ Human repeats ☐ Mask for lookup table only ☐ Mask lower case

Expect   [10   ]

Word Size   [11 ▼]

Other advanced   [   ]

Format

Show   ☑ Graphical Overview ☑ Linkout ☑ Sequence Retrieval ☑ NCBI-gi [Alignment ▼] in [HTML ▼] format

☐ CDS feature

Masking Character [Lower Case   ▼] Masking Color [Grey ▼]

Number of: Descriptions [100 ▼] Alignments [50 ▼] Graphic overview [100 ▼]

Alignment view   [Pairwise   ▼]

Limit results by entrez query   [   ] or select from: [All organisms   ▼]

http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi

NCBI *formatting* **BLAST**

Nucleotide   Protein   Translations   Retrieve results for an RID

Your request has been successfully submitted and put into the Blast Queue.

Query = (29,742 letters)

The request ID is | 1151086129-31006-68807045580.BLASTQ4

[Format!] or [Reset!]

The results are estimated to be ready in 14 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☑ Graphical Overview ☑ Linkout ☑ Sequence Retrieval ☑ NCBI-gi | Alignment ▼ | in | HTML ▼ | format

☐ CDS feature

Masking Character | Lower Case ▼ | Masking Color | Grey ▼

Number of: Descriptions | 100 ▼ | Alignments | 50 ▼ | Graphic overview | 100 ▼

Alignment view | Pairwise ▼

Limit results by entrez query | | or select from: | All organisms ▼

Expect value range: | |

BLASTN 2.2.14 [May-07-2006]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman
(1997), "Gapped BLAST and PSI-BLAST: a new generation of
protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1151086129-31006-68807045580.BLASTQ4

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,
GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)
          4,084,561 sequences; 17,475,977,371 total letters

If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**

Taxonomy reports

Query=
Length=29742

Distribution of 226 Blast Hits on the Query Sequence

Mouse-over to show defline and scores, click to show alignments

Color key for alignment scores

<40	40-50	50-80	80-200	>=200

Query

0	5500	11000	16500	22000	27500
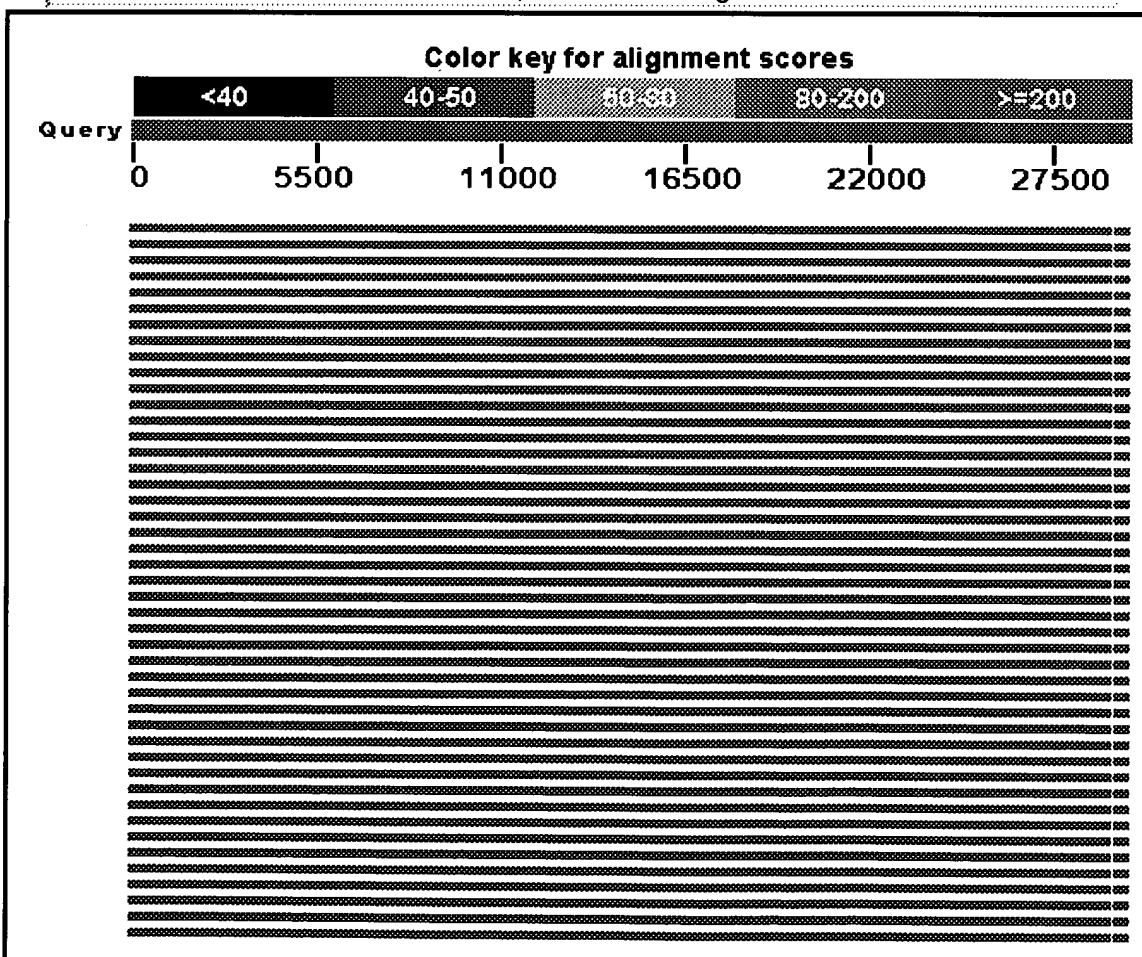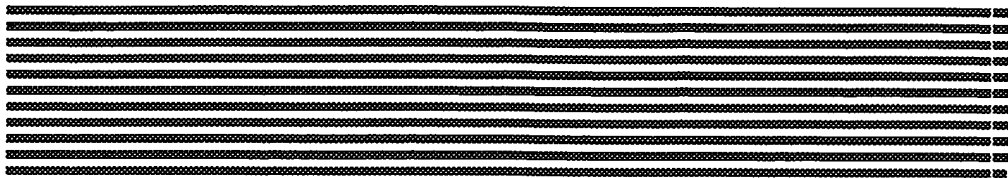
Distance tree of results NEW

Sequences producing significant alignments:	Score (Bits)	E Value
gi|30023963|gb|AY278491.2| SARS coronavirus HKU-39849, complete	5.785e+04	0.0
gi|33115118|gb|AY323977.2| SARS coronavirus HSR 1, complete geno	5.777e+04	0.0
gi|30698326|gb|AY291451.1| SARS coronavirus TW1, complete genome	5.777e+04	0.0
gi|40548933|gb|AY502928.1| SARS coronavirus TW5, complete genome	5.777e+04	0.0
gi|40548897|gb|AY502925.1| SARS coronavirus TW2, complete genome	5.777e+04	0.0
gi|52546959|gb|AY714217.1| SARS Coronavirus CDC#200301157, compl	5.776e+04	0.0
gi|30248028|gb|AY274119.3| SARS coronavirus TOR2, complete genom	5.776e+04	0.0
gi|31873092|gb|AY321118.1| SARS coronavirus TWC, complete genome	5.775e+04	0.0
gi|40548945|gb|AY502929.1| SARS coronavirus TW6, complete genome	5.775e+04	0.0
gi|40548921|gb|AY502927.1| SARS coronavirus TW4, complete genome	5.775e+04	0.0
gi|40548909|gb|AY502926.1| SARS coronavirus TW3, complete genome	5.775e+04	0.0
gi|33518725|gb|AY362699.1| SARS coronavirus TWC3, complete genom	5.775e+04	0.0
gi|40548969|gb|AY502931.1| SARS coronavirus TW8, complete genome	5.775e+04	0.0
gi|40548957|gb|AY502930.1| SARS coronavirus TW7, complete genome	5.774e+04	0.0
gi|37576845|gb|AY427439.1| SARS coronavirus AS, complete genome	5.774e+04	0.0
gi|33518724|gb|AY362698.1| SARS coronavirus TWC2, complete genom	5.774e+04	0.0
gi|33411399|dbj|AP006557.1| SARS coronavirus TWH genomic RNA, co	5.774e+04	0.0
gi|37624341|gb|AY394998.1| SARS coronavirus LC1, complete genome	5.774e+04	0.0
gi|30027617|gb|AY278741.1| SARS coronavirus Urbani, complete gen	5.774e+04	0.0
gi|31581502|gb|AY291315.1| SARS coronavirus Frankfurt 1, complet	5.774e+04	0.0
gi|33578015|gb|AY310120.1| SARS coronavirus FRA, complete genome	5.774e+04	0.0
gi|40548981|gb|AY502932.1| SARS coronavirus TW9, complete genome	5.773e+04	0.0
gi|38304867|gb|AY282752.2| SARS coronavirus CUHK-Su10, complete	5.773e+04	0.0
gi|38505491|gb|AY485278.1| SARS coronavirus Sino3-11, complete g	5.773e+04	0.0
gi|40548873|gb|AY502923.1| SARS coronavirus TW10, complete genom	5.773e+04	0.0
gi|30468042|gb|AY283794.1| SARS coronavirus Sin2500, complete ge	5.773e+04	0.0
gi|30468044|gb|AY283796.1| SARS coronavirus Sin2679, complete ge	5.773e+04	0.0
gi|33411459|dbj|AP006561.1| SARS coronavirus TWY genomic RNA, co	5.773e+04	0.0
gi|33411444|dbj|AP006560.1| SARS coronavirus TWS genomic RNA, co	5.773e+04	0.0
gi|38231927|gb|AY350750.1| SARS coronavirus PUMC01, complete gen	5.773e+04	0.0
gi|33114202|gb|AY345987.1| SARS coronavirus CUHK-AG02, complete	5.772e+04	0.0
gi|33114190|gb|AY345986.1| SARS coronavirus CUHK-AG01, complete	5.772e+04	0.0
gi|67003761|gb|AY864805.1| SARS coronavirus BJ162, complete geno	5.772e+04	0.0
gi|33411429|dbj|AP006559.1| SARS coronavirus TWK genomic RNA, co	5.772e+04	0.0
gi|37361915|gb|AY283798.2| SARS coronavirus Sin2774, complete ge	5.771e+04	0.0
gi|38231932|gb|AY357075.1| SARS coronavirus PUMC02, complete gen	5.771e+04	0.0
gi|37624333|gb|AY394990.1| SARS coronavirus HZS2-E, complete gen	5.771e+04	0.0
gi|37624332|gb|AY394989.1| SARS coronavirus HZS2-D, complete gen	5.771e+04	0.0
gi|33114214|gb|AY345988.1| SARS coronavirus CUHK-AG03, complete	5.771e+04	0.0
gi|33411414|dbj|AP006558.1| SARS coronavirus TWJ genomic RNA, co	5.771e+04	0.0
gi|38505482|gb|AY485277.1| SARS coronavirus Sino1-11, complete g	5.770e+04	0.0
gi|45644994|gb|AY559081.1| SARS coronavirus Sin842, complete gen	5.770e+04	0.0
gi|37624334|gb|AY394991.1| SARS coronavirus HZS2-Fc, complete ge	5.770e+04	0.0
gi|67003775|gb|AY864806.1| SARS coronavirus BJ202, complete geno	5.770e+04	0.0
gi|45645004|gb|AY559087.1| SARS coronavirus Sin3725V, complete g	5.769e+04	0.0
gi|45645023|gb|AY559096.1| SARS coronavirus Sin850, complete gen	5.769e+04	0.0
gi|37624336|gb|AY394993.1| SARS coronavirus HGZ8L2, complete gen	5.769e+04	0.0
gi|37624335|gb|AY394992.1| SARS coronavirus HZS2-C, complete gen	5.769e+04	0.0
gi|30468045|gb|AY283797.1| SARS coronavirus Sin2748, complete ge	5.769e+04	0.0
gi|38231937|gb|AY357076.1| SARS coronavirus PUMC03, complete gen	5.769e+04	0.0

gi|45645007|gb|AY559088.1|	SARS coronavirus SinP1, complete geno	5.768e+04	0.0
gi|99078934|gb|DQ497008.1|	SARS coronavirus strain MA-15, comple	5.768e+04	0.0
gi|74275570|gb|DQ182595.1|	SARS coronavirus ZJ0301 from China, c	5.768e+04	0.0
gi|45645017|gb|AY559092.1|	SARS coronavirus SinP5, complete geno	5.768e+04	0.0
gi|40548885|gb|AY502924.1|	SARS coronavirus TW11, complete genom	5.768e+04	0.0
gi|38385714|gb|AY461660.1|	SARS coronavirus SoD, complete genome	5.768e+04	0.0
gi|30468043|gb|AY283795.1|	SARS coronavirus Sin2677, complete ge	5.768e+04	0.0
gi|30027610|gb|AY278554.2|	SARS coronavirus CUHK-W1, complete ge	5.768e+04	0.0
gi|45645000|gb|AY559084.1|	SARS coronavirus Sin3765V, complete g	5.767e+04	0.0
gi|45645022|gb|AY559095.1|	SARS coronavirus Sin847, complete gen	5.767e+04	0.0
gi|34482146|gb|AY304495.1|	SARS coronavirus GZ50, complete genom	5.767e+04	0.0
gi|45645019|gb|AY559093.1|	SARS coronavirus Sin845, complete gen	5.767e+04	0.0
gi|45645016|gb|AY559091.1|	SARS coronavirus SinP4, complete geno	5.766e+04	0.0
gi|45645001|gb|AY559085.1|	SARS coronavirus Sin848, complete gen	5.766e+04	0.0
gi|37624330|gb|AY394987.1|	SARS coronavirus HZS2-Fb, complete ge	5.765e+04	0.0
gi|40795428|gb|AY394850.2|	SARS coronavirus WHU, complete genome	5.765e+04	0.0
gi|50365700|gb|AY654624.1|	SARS coronavirus TJF, complete genome	5.765e+04	0.0
gi|30275666|gb|AY278488.2|	SARS coronavirus BJ01, complete genom	5.764e+04	0.0
gi|37624326|gb|AY394983.1|	SARS coronavirus HSZ2-A, complete gen	5.764e+04	0.0
gi|40795744|gb|AY508724.1|	SARS coronavirus NS-1, complete genom	5.763e+04	0.0
gi|31416306|gb|AY279354.2|	SARS coronavirus BJ04, complete genom	5.763e+04	0.0
gi|31416292|gb|AY278487.3|	SARS coronavirus BJ02, complete genom	5.761e+04	0.0
gi|32493129|gb|AY338174.1|	SARS coronavirus Taiwan TC1, complete	5.761e+04	0.0
gi|31416305|gb|AY278490.3|	SARS coronavirus BJ03, complete genom	5.759e+04	0.0
gi|33188324|gb|AY348314.1|	SARS coronavirus Taiwan TC3, complete	5.758e+04	0.0
gi|32493130|gb|AY338175.1|	SARS coronavirus Taiwan TC2, complete	5.757e+04	0.0
gi|108597802|gb|DQ640652.1|	SARS coronavirus GDH-BJH01, complete	5.756e+04	0.0
gi|45645013|gb|AY559090.1|	SARS coronavirus SinP3, complete geno	5.756e+04	0.0
gi|49176846|gb|AY595412.1|	SARS coronavirus LLJ-2004, complete g	5.755e+04	0.0
gi|45645010|gb|AY559089.1|	SARS coronavirus SinP2, complete geno	5.720e+04	0.0
gi|37624337|gb|AY394994.1|	SARS coronavirus HSZ-Bc, complete gen	5.498e+04	0.0
gi|37624338|gb|AY394995.1|	SARS coronavirus HSZ-Cc, complete gen	5.496e+04	0.0
gi|37624329|gb|AY394986.1|	SARS coronavirus HSZ-Cb, complete gen	5.489e+04	0.0
gi|45644996|gb|AY559082.1|	SARS coronavirus Sin852, complete gen	5.484e+04	0.0
gi|41323719|gb|AY390556.1|	SARS coronavirus GZ02, complete genom	5.484e+04	0.0
gi|45644998|gb|AY559083.1|	SARS coronavirus Sin3408, complete ge	5.482e+04	0.0
gi|45645003|gb|AY559086.1|	SARS coronavirus Sin849, complete gen	5.481e+04	0.0
gi|37624340|gb|AY394997.1|	SARS coronavirus ZS-A, complete genom	5.476e+04	0.0
gi|37624339|gb|AY394996.1|	SARS coronavirus ZS-B, complete genom	5.476e+04	0.0
gi|37624344|gb|AY395001.1|	SARS coronavirus LC4, complete genome	5.473e+04	0.0
gi|37624343|gb|AY395000.1|	SARS coronavirus LC3, complete genome	5.473e+04	0.0
gi|37624345|gb|AY395002.1|	SARS coronavirus LC5, complete genome	5.473e+04	0.0
gi|37624342|gb|AY394999.1|	SARS coronavirus LC2, complete genome	5.473e+04	0.0
gi|37624321|gb|AY394978.1|	SARS coronavirus GZ-B, complete genom	5.472e+04	0.0
gi|34482137|gb|AY304486.1|	SARS coronavirus SZ3, complete genome	5.470e+04	0.0
gi|37624322|gb|AY394979.1|	SARS coronavirus GZ-C, complete genom	5.468e+04	0.0
gi|45645021|gb|AY559094.1|	SARS coronavirus Sin846, complete gen	5.459e+04	0.0
gi|92698732|dbj|AB257344.1|	SARS coronavirus Frankfurt 1 geno...	5.423e+04	0.0
gi|60267744|gb|AY772062.1|	SARS coronavirus WH20, complete genom	5.391e+04	0.0
gi|39980888|gb|AY286320.4|	SARS coronavirus ZJ01, partial genome	5.199e+04	0.0

Alignments

Get selected sequences	Select all	Deselect all	Tree View

> ☐ gi\|30023963\|gb\|AY278491.2\| ▨ SARS coronavirus HKU-39849, complete genome
Length=29742

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 Score = 5.785e+04 bits (29181),  Expect = 0.0
 Identities = 29226/29226 (100%), Gaps = 0/29226 (0%)
 Strand=Plus/Plus
```

```
Query  1     ATATTAGGTTTTTACCTACCCAGGAAAAGCCAACCAACCTCGATCTCTTGTAGATCTGTT  60
```

. http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi

```
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1     ATATTAGGTTTTTACCTACCCAGGAAAAGCCAACCAACCTCGATCTCTTGTAGATCTGTT   60

Query   61    CTCTAAACGAACTTTAAAATCTGTGTAGCTGTCGCTCGGCTGCATGCCTAGTGCACCTAC   120
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61    CTCTAAACGAACTTTAAAATCTGTGTAGCTGTCGCTCGGCTGCATGCCTAGTGCACCTAC   120

Query   121   GCAGTATAAACAATAATAAATTTTACTGTCGTTGACAAGAAACGAGTAACTCGTCCCTCT   180
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121   GCAGTATAAACAATAATAAATTTTACTGTCGTTGACAAGAAACGAGTAACTCGTCCCTCT   180

Query   181   TCTGCAGACTGCTTACGGTTTCGTCCGTGTTGCAGTCGATCATCAGCATACCTAGGTTTC   240
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181   TCTGCAGACTGCTTACGGTTTCGTCCGTGTTGCAGTCGATCATCAGCATACCTAGGTTTC   240

Query   241   GTCCGGGTGTGACCGAAAGGTAAGATGGAGAGCCTTGTTCTTGGTGTCAACGAGAAAACA   300
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241   GTCCGGGTGTGACCGAAAGGTAAGATGGAGAGCCTTGTTCTTGGTGTCAACGAGAAAACA   300
```

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? ds

Set      Items    Description
S1        3809    SARS
S2           0    PD>2004
S3     1532886    PY>2003
S4        2213    S1 AND S3
S5       88358    PUTATIVE
S6          33    S4 AND S5
? log hold
      23jun06 12:35:54 User208669 Session D3045.2
          $17.86    5.253 DialUnits File155
               $0.00  33 Type(s) in Format  6
               $2.42  11 Type(s) in Format  7
           $2.42  44 Types
    $20.28  Estimated cost File155
     $2.66  TELNET
    $22.94  Estimated cost this search
    $23.86  Estimated total session cost   5.511 DialUnits
Logoff: level 05.12.03 D  12:35:54
```